In the Specification:

Please replace the paragraph at page 15, lines 25-37, with the following replacement paragraph:

The percent identity between two nucleotide sequences can be determined using the GAP program in the GCG software package (available at the Genetics Computer Group (GCG) website ~~http://www.gcg.com~~), using a NWSgapdna.CMP matrix and a gap weight of 40, 50, 60, 70, or 80 and a length weight of 1, 2, 3, 4, 5, or 6. The percent identity between two nucleotide or amino acid sequences can also determined using the algorithm of E. Meyers and W. Miller (*Comput. Appl. Biosci.*, 4:11-17 (1988)) which has been incorporated into the ALIGN program (version 2.0), using a PAM120 weight residue table, a gap length penalty of 12 and a gap penalty of 4. In addition, the percent identity between two amino acid sequences can be determined using the Needleman and Wunsch (*J. Mol. Biol.* (48):444-453 (1970)) algorithm which has been incorporated into the GAP program in the GCG software package ~~(available at http://www.gcg.com)~~, using either a Blossum 62 matrix or a PAM250 matrix, and a gap weight of 16, 14, 12, 10, 8, 6, or 4 and a length weight of 1, 2, 3, 4, 5, or 6.

Please replace the paragraph at page 16, lines 1-13, with the following replacement paragraph:

The nucleic acid and protein sequences of the present invention can further be used as a "query sequence" to perform a search against public databases to, for example, identify related sequences. Such searches can be performed using the NBLAST and XBLAST programs (version 2.0) of Altschul, et al. (1990) *J. Mol. Biol.* 215:403-10. BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to the nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to the protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul et al., (1997) *Nucleic Acids Res.* 25(17):3389-3402. When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (*e.g.*, XBLAST and NBLAST) can be used. See the web site of the National Center for Biotechnology Information ~~http://www.ncbi.nlm.nih.gov~~.

Please replace the paragraph at page 64, lines 14-21, with the following replacement paragraph:

The N-terminal microsequencing results of the monoclonal antibody B11 target antigen revealed the following protein sequence: LLDTR QFLIY LEDTK RCVDA (SEQ ID NO:7). This sequence again matched that of the human macrophage mannose receptor (GenBank Accession # NP_002429) with 100% identity over 20 amino acids as determined using the BLAST algorithm at the National Center for Biotechnology Information web site (~~http://www.ncbi.nlm.nih.gov/~~). These data indicate that the target molecule on dendritic cells recognized by human monoclonal antibody B11 is the macrophage mannose receptor.